Figure 1

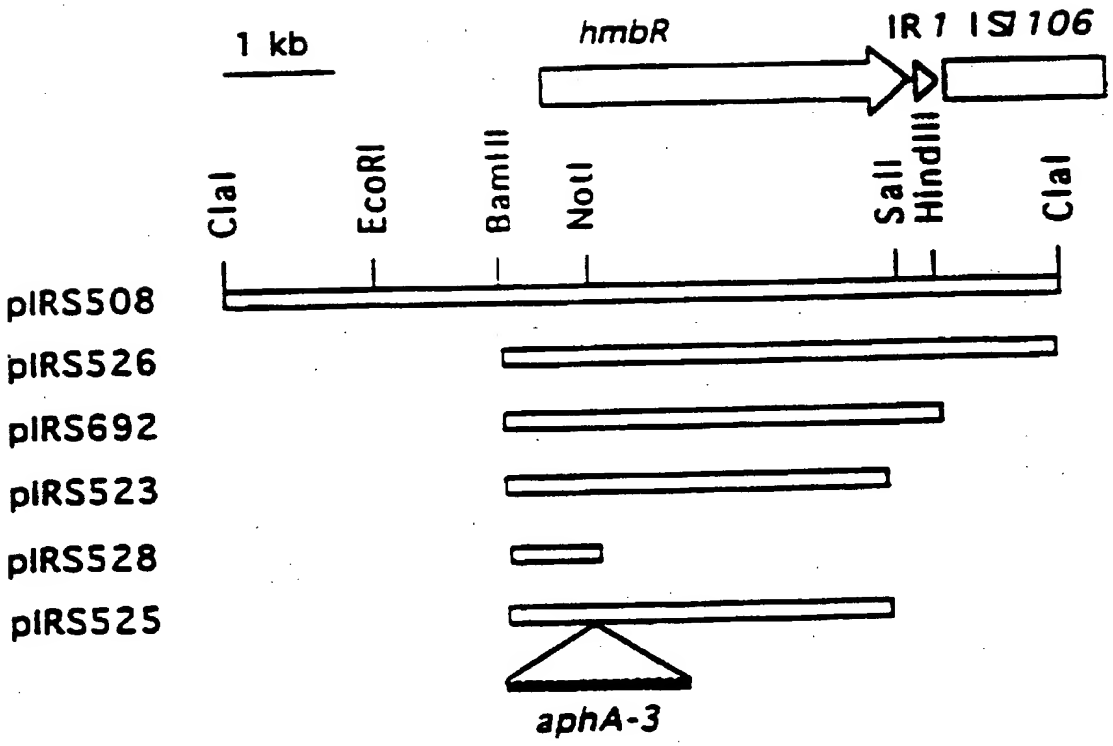

1 kb
hmbR
IR 1 IS 106
ClaI
EcoRI
BamHI
NotI
SalI
HindIII
ClaI
pIRS508
pIRS526
pIRS692
pIRS523
pIRS528
pIRS525
aphA-3

FIG. 2A


10
60
AGAACTAGTGGATCCAATTTGGGCGCGGCGTTTTTGTTCAAACACGCCCAAAAACTCGAT
BamHI
110
TACAACGGCGAACACGGCGCGCGCCACCTCGCTCCGCATCCCGACGGGCCGCGGCAAACA
160
CTGGCGCGCCTTCGTCGAGCATCTGAACGCTTTGAACCTGACTCCCGAAGCCGAAGCGGA
210
AGCCATTCAAGGCGCGCGCGAAGCCTTTGCATTCTACAAAGTCGTGTTGCGCGAAACCTT
260
CGGCTTGGCAGCCGATGCCGAAGCCCCCGAAGGTATGATGCCGCACAGGCACTAAAAAAT
310
360
AATCGAACCAAATAAACAAGGTCTCGGCATAGCTGTTTGCAGGGACCTTTAATTACACGG
-10
410
CGCGGCTTTGTTTACATGGATTACTGTCTTATTAAATATTAATGATTATCATAAAATCTA
Fur-box
TTATTCGCTAACCGATGGATGAACAATCCATACATCTTGAGTTGATAATATGAAACCATT
SD
MetLysPrcLe

FIG. 2B

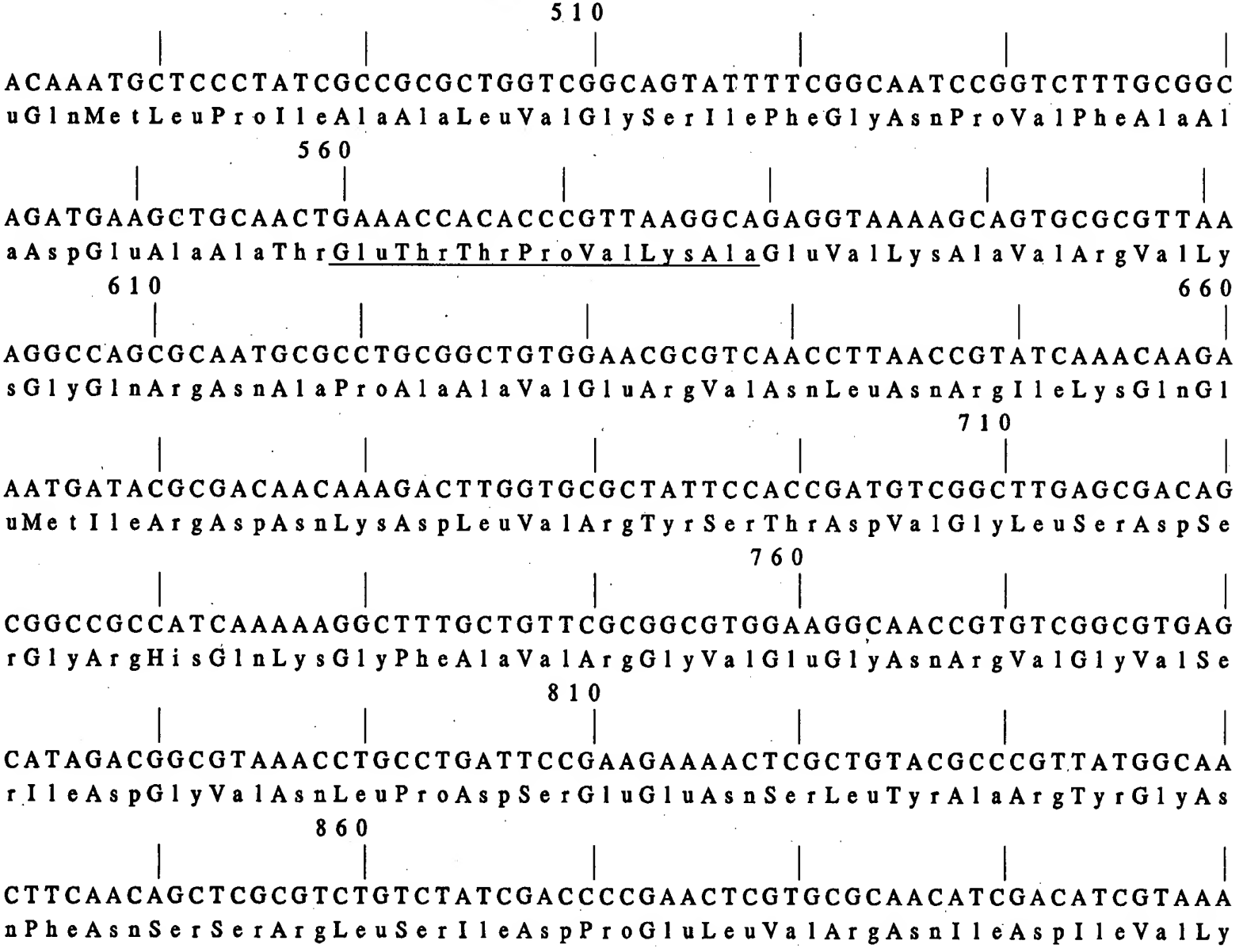

510
ACAAATGCTCCCTATCGCCGCGCTGGTCGGCAGTATTTTCGGCAATCCGGTCTTTGCGGC
uGlnMetLeuProIleAlaAlaLeuValGlySerIlePheGlyAsnProValPheAlaAl
560
AGATGAAGCTGCAACTGAAACCACACCCGTTAAGGCAGAGGTAAAAGCAGTGCGCGTTAA
aAspGluAlaAlaThrGluThrThrProValLysAlaGluValLysAlaValArgValLy
610
660
AGGCCAGCGCAATGCGCCTGCGGCTGTGGAACGCGTCAACCTTAACCGTATCAAACAAGA
sGlyGlnArgAsnAlaProAlaAlaValGluArgValAsnLeuAsnArgIleLysGlnGl
710
AATGATACGCGACAACAAAGACTTGGTGCGCTATTCCACCGATGTCGGCTTGAGCGACAG
uMetIleArgAspAsnLysAspLeuValArgTyrSerThrAspValGlyLeuSerAspSe
760
CGGCCGCCATCAAAAAGGCTTTGCTGTTCGCGGCGTGGAAGGCAACCGTGTCGGCGTGAG
rGlyArgHisGlnLysGlyPheAlaValArgGlyValGluGlyAsnArgValGlyValSe
810
CATAGACGGCGTAAACCTGCCTGATTCCGAAGAAAACTCGCTGTACGCCCGTTATGGCAA
rIleAspGlyValAsnLeuProAspSerGluGluAsnSerLeuTyrAlaArgTyrGlyAs
860
CTTCAACAGCTCGCGTCTGTCTATCGACCCCGAACTCGTGCGCAACATCGACATCGTAAA
nPheAsnSerSerArgLeuSerIleAspProGluLeuValArgAsnIleAspIleValLy

FIG. 2C

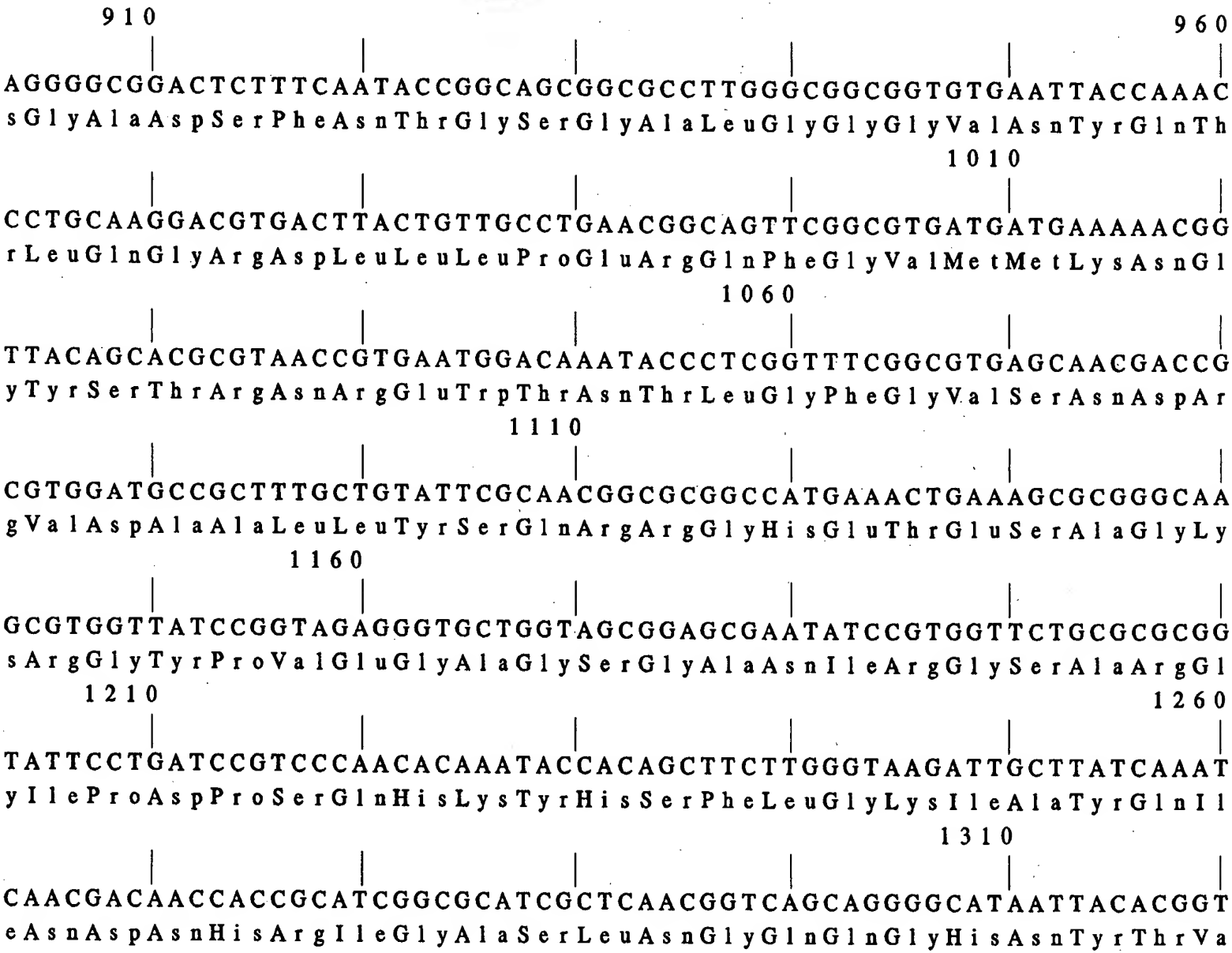

910
960
AGGGGCGGACTCTTTCAATACCGGCAGCGGCGCCTTGGGCGGCGGTGTGAATTACCAAAC
sGlyAlaAspSerPheAsnThrGlySerGlyAlaLeuGlyGlyGlyValAsnTyrGlnTh
1010
CCTGCAAGGACGTGACTTACTGTTGCCTGAACGGCAGTTCGGCGTGATGATGAAAAACGG
rLeuGlnGlyArgAspLeuLeuLeuProGluArgGlnPheGlyValMetMetLysAsnGl
1060
TTACAGCACGCGTAACCGTGAATGGACAAATACCCTCGGTTTCGGCGTGAGCAACGACCG
yTyrSerThrArgAsnArgGluTrpThrAsnThrLeuGlyPheGlyValSerAsnAspAr
1110
CGTGGATGCCGCTTTGCTGTATTCGCAACGGCGCGGCCATGAAACTGAAAGCGCGGGCAA
gValAspAlaAlaLeuLeuTyrSerGlnArgArgGlyHisGluThrGluSerAlaGlyLy
1160
GCGTGGTTATCCGGTAGAGGGTGCTGGTAGCGGAGCGAATATCCGTGGTTCTGCGCGCGG
sArgGlyTyrProValGluGlyAlaGlySerGlyAlaAsnIleArgGlySerAlaArgGl
1210
1260
TATTCCTGATCCGTCCCAACACAAATACCACAGCTTCTTGGGTAAGATTGCTTATCAAAT
yIleProAspProSerGlnHisLysTyrHisSerPheLeuGlyLysIleAlaTyrGlnIl
1310
CAACGACAACCACCGCATCGGCGCATCGCTCAACGGTCAGCAGGGGCATAATTACACGGT
eAsnAspAsnHisArgIleGlyAlaSerLeuAsnGlyGlnGlnGlyHisAsnTyrThrVa

FIG. 2D

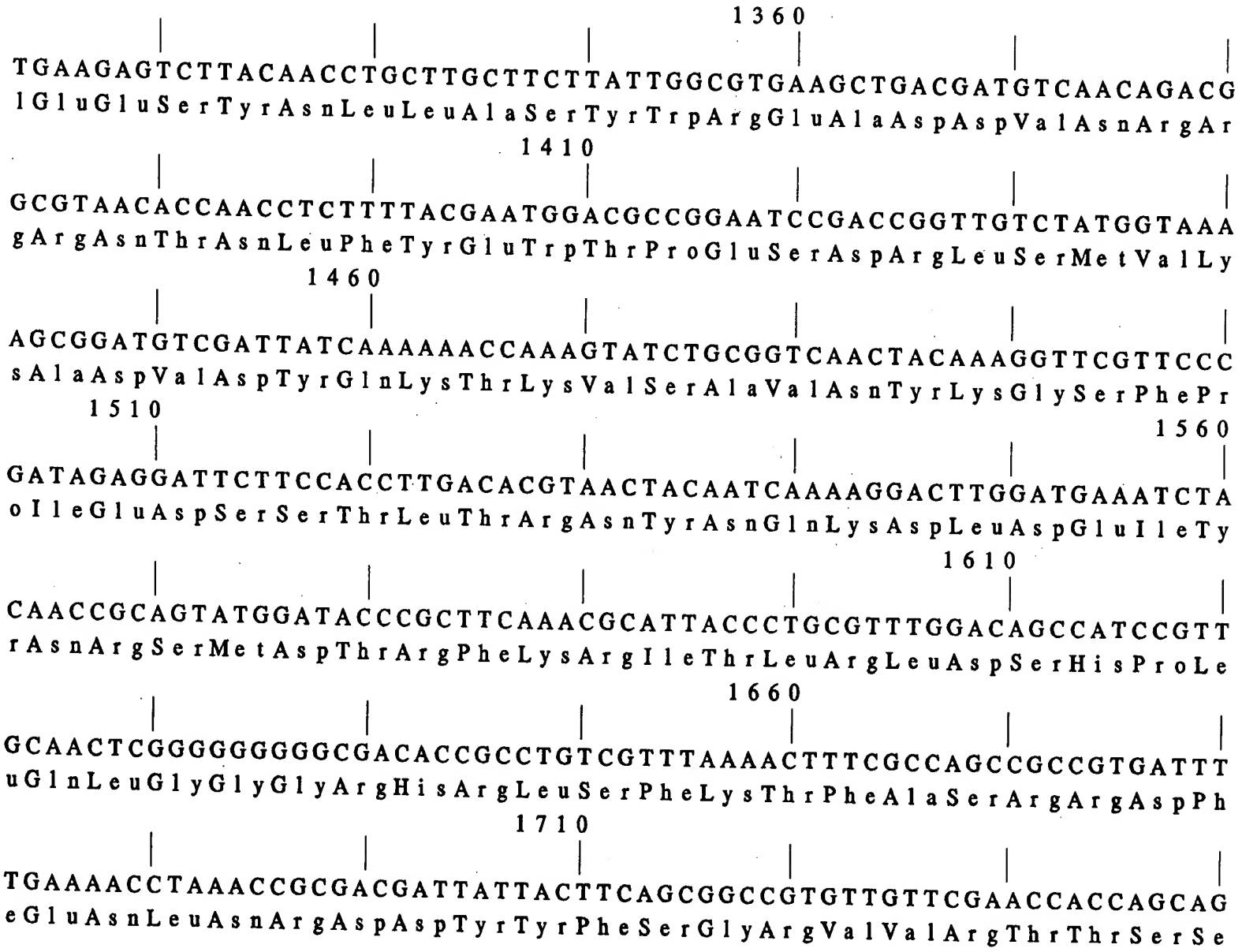


FIG. 2E


1760
TATCCAGCATCCGGTGAAAACCACCAACTACGGTTTCTCACTGTCTGACCAAATTCAATG
rIleGlnHisProValLysThrThrAsnTyrGlyPheSerLeuSerAspGlnIleGlnTr
1810
1860
GAACGACGTGTTCAGTAGCCGCGCAGGTATCCGTTACGATCATACCAAAATGACGCCTCA
pAsnAspValPheSerSerArgAlaGlyIleArgTyrAspHisThrLysMETThrProGl
1910
GGAATTGAATGCCGAGTGTCATGCTTGTGACAAAACACCGCCTGCAGCCAACACTTATAA
nGluLeuAsnAlaGluCysHisAlaCysAspLysThrProProAlaAlaAsnThrTyrLy
1960
AGGCTGGAGCGGTTTTGTCGGCTTGGCGGCGCAACTGAATCAGGCTTGGCGTGTCGGTTA
sGlyTrpSerGlyPheValGlyLeuAlaAlaGluLeuAsaGluAlaTrpArgValGlyTy
2010
CGACATTACTTCCGGCTACCGTGTCCCCAATGCGTCCGAAGTGTATTTCACTTACAACCA
rAspIleThrSerGlyTyrArgValProAsnAlaSerGluValTyrPheThrTyrAsnHi
2060
CGGTTCGGGTAATTGGCTGCCCAATCCCAACCTGAAAGCCGAGCGCACGACCACCCACAC
sGlySerGlyAsnTrpLeuProAsnProAsnLeuLysAlaGluArgThrThrThrHisTh
2110
2160
CCTCTCTCTGCAAGGCCGCAGCGAAAAAGGTACTTTGGATGCCAACCTGTATCAAAGCAA
rLeuSerLeuGlnGlyArgSerGluLysGlyThrLeuAspAlaAsnLeuTyrGlnSerAs

FIG. 2F

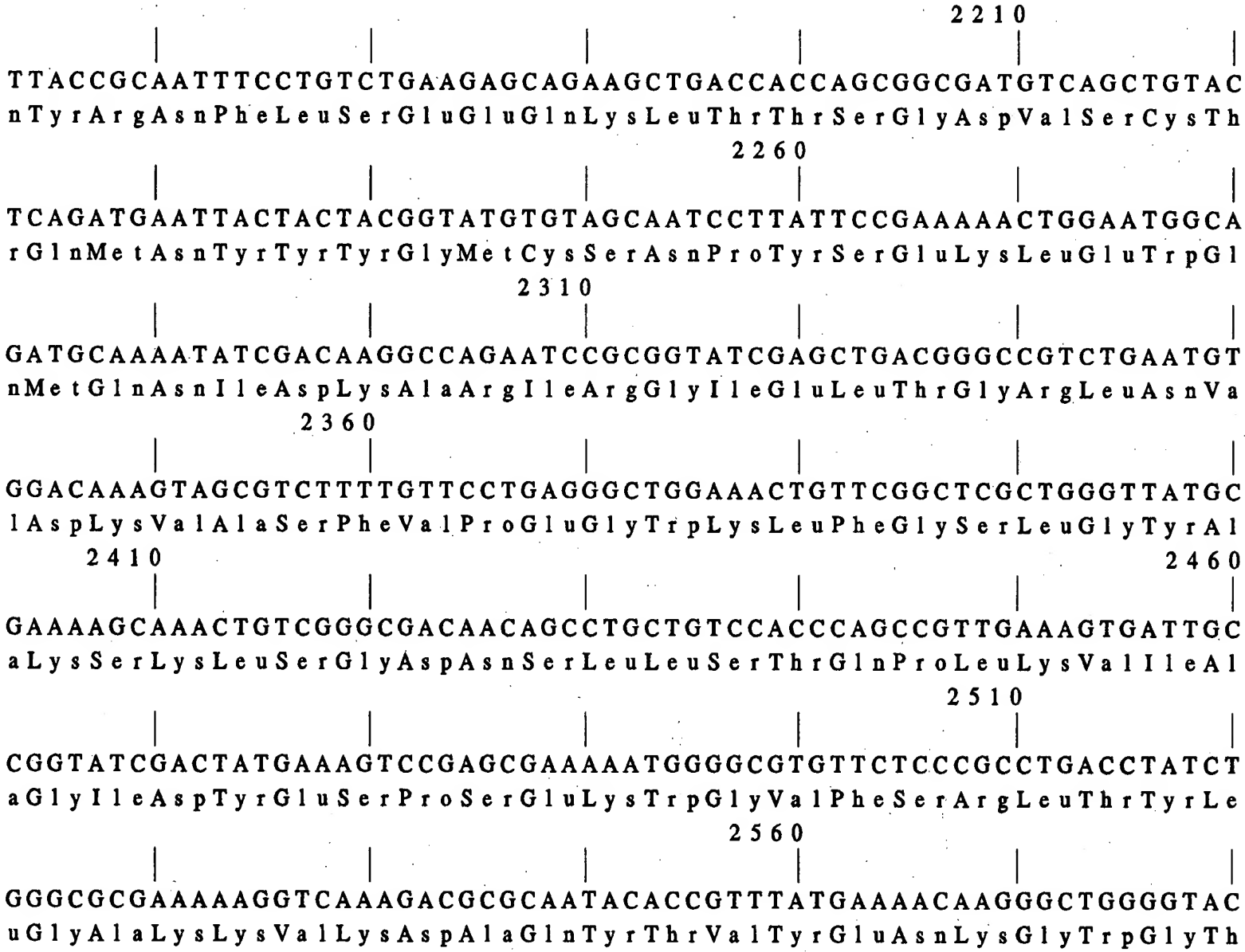

2210
TTACCGCAATTTCCTGTCTGAAGAGCAGAAGCTGACCACCAGCGGCGATGTCAGCTGTAC
nTyrArgAsnPheLeuSerGluGluGlnLysLeuThrThrSerGlyAspValSerCysTh
2260
TCAGATGAATTACTACTACGGTATGTGTAGCAATCCTTATTCCGAAAAACTGGAATGGCA
rGlnMetAsnTyrTyrTyrGlyMetCysSerAsnProTyrSerGluLysLeuGluTrpGl
2310
GATGCAAAATATCGACAAGGCCAGAATCCGCGGTATCGAGCTGACGGGCCGTCTGAATGT
nMetGlnAsnIleAspLysAlaArgIleArgGlyIleGluLeuThrGlyArgLeuAsnVa
2360
GGACAAAGTAGCGTCTTTTGTTCCTGAGGGCTGGAAACTGTTCGGCTCGCTGGGTTATGC
lAspLysValAlaSerPheValProGluGlyTrpLysLeuPheGlySerLeuGlyTyrAl
2410
2460
GAAAAGCAAACTGTCGGGCGACAACAGCCTGCTGTCCACCCAGCCGTTGAAAGTGATTGC
aLysSerLysLeuSerGlyAspAsnSerLeuLeuSerThrGlnProLeuLysValIleAl
2510
CGGTATCGACTATGAAAGTCCGAGCGAAAAATGGGGCGTGTTCTCCCGCCTGACCTATCT
aGlyIleAspTyrGluSerProSerGluLysTrpGlyValPheSerArgLeuThrTyrLe
2560
GGGCGCGAAAAAGGTCAAAGACGCGCAATACACCGTTTATGAAAACAAGGGCTGGGGTAC
uGlyAlaLysLysValLysAspAlaGlnTyrThrValTyrGluAsnLysGlyTrpGlyTh

FIG. 2G

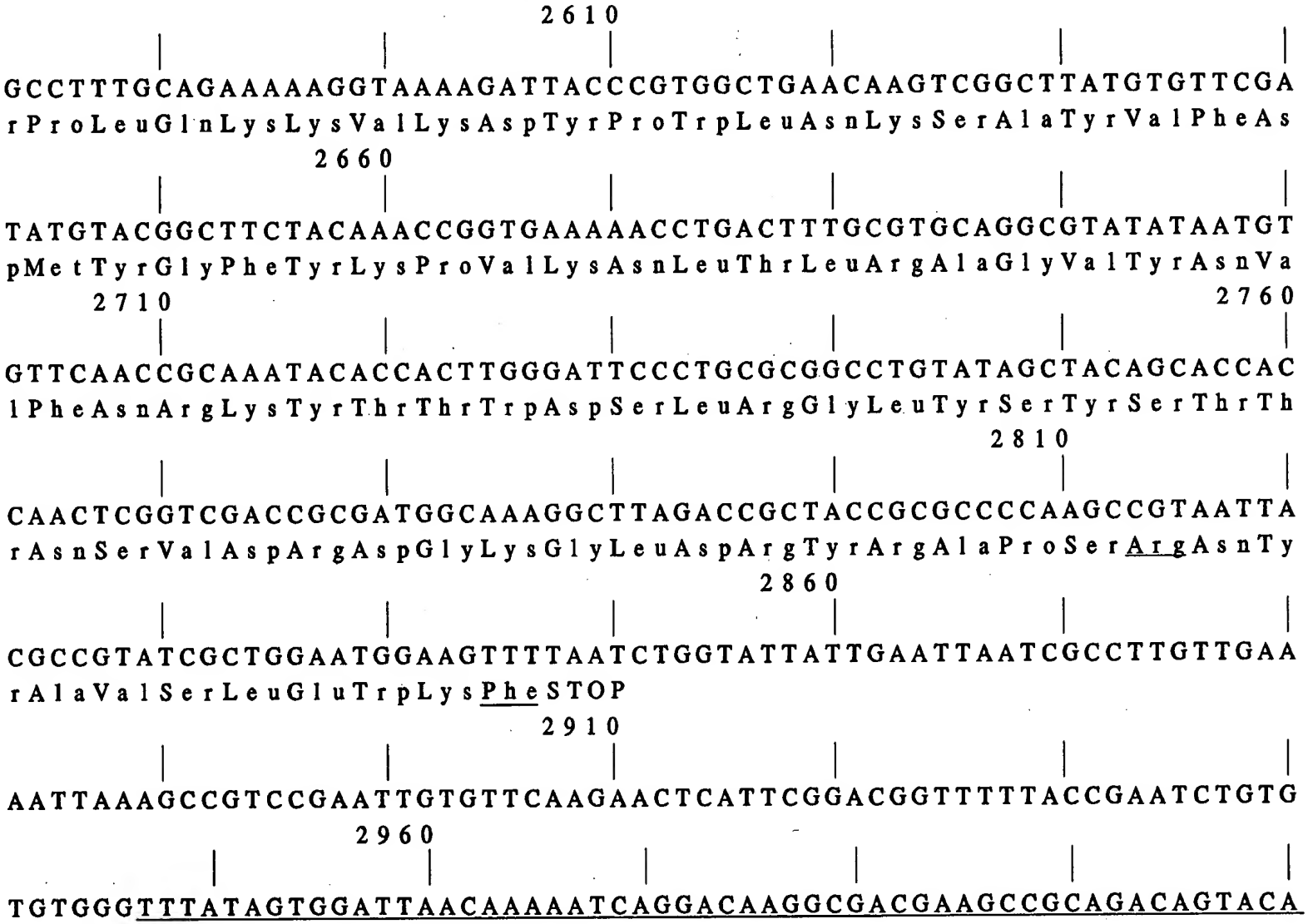
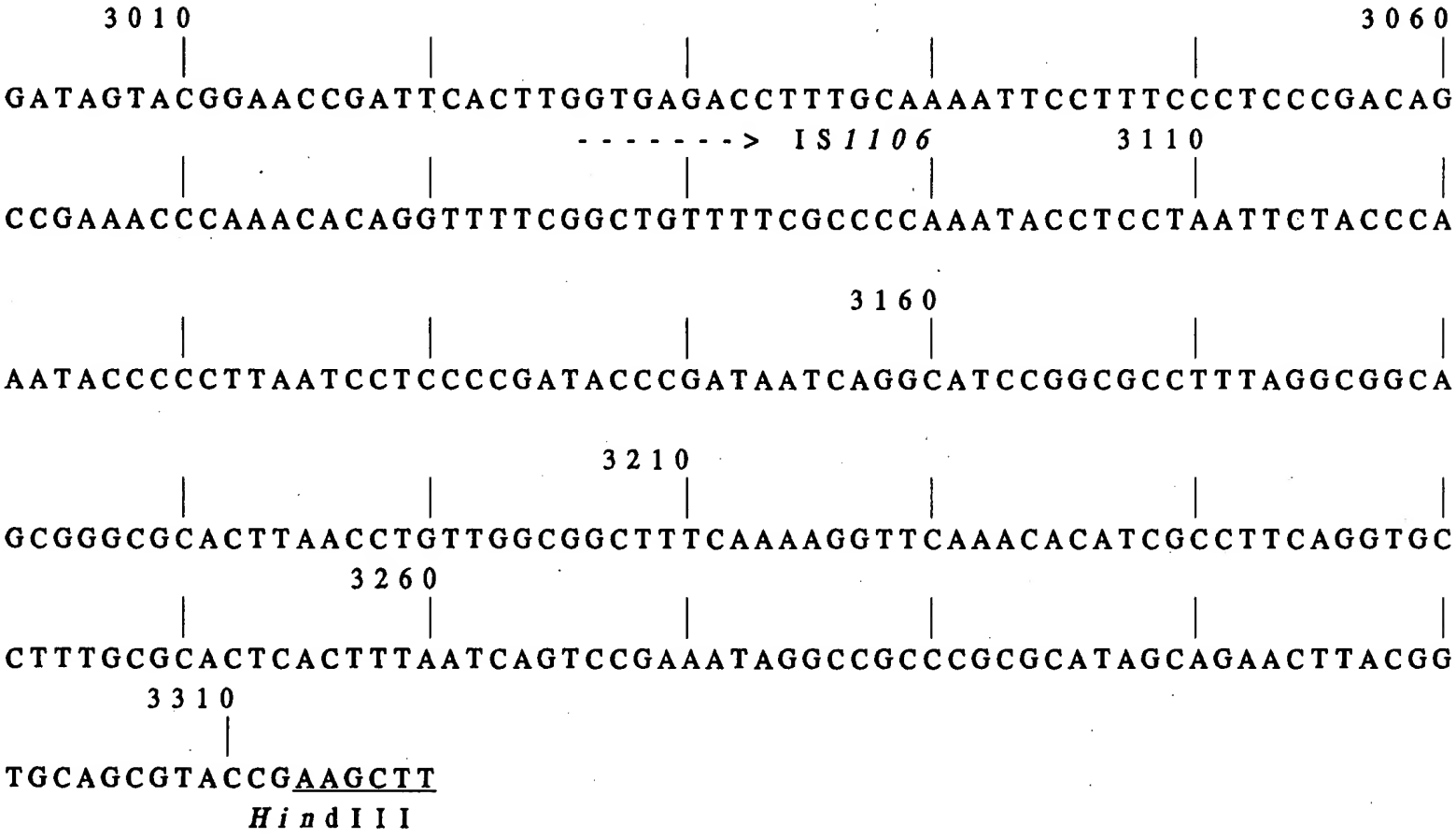

2610
GCCTTTGCAGAAAAAGGTAAAAGATTACCCGTGGCTGAACAAGTCGGCTTATGTGTTCGA
rProLeuGlnLysLysValLysAspTyrProTrpLeuAsnLysSerAlaTyrValPheAs
2660
TATGTACGGCTTCTACAAACCGGTGAAAAACCTGACTTTGCGTGCAGGCGTATATAATGT
pMetTyrGlyPheTyrLysProValLysAsnLeuThrLeuArgAlaGlyValTyrAsnVa
2710
2760
GTTCAACCGCAAATACACCACTTGGGATTCCCTGCGCGGCCTGTATAGCTACAGCACCAC
lPheAsnArgLysTyrThrThrTrpAspSerLeuArgGlyLeuTyrSerTyrSerThrTh
2810
CAACTCGGTCGACCGCGATGGCAAAGGCTTAGACCGCTACCGCGCCCCAAGCCGTAATTA
rAsnSerValAspArgAspGlyLysGlyLeuAspArgTyrArgAlaProSerArgAsnTy
2860
CGCCGTATCGCTGGAATGGAAGTTTTAATCTGGTATTATTGAATTAATCGCCTTGTTGAA
rAlaValSerLeuGluTrpLysPheSTOP
2910
AATTAAAGCCGTCCGAATTGTGTTCAAGAACTCATTCGGACGGTTTTTACCGAATCTGTG
2960
TGTGGGTTTATAGTGGATTAACAAAAATCAGGACAAGGCGACGAAGCCGCAGACAGTACA

FIG. 2H


3010
3060
GATAGTACGGAACCGATTCACTTGGTGAGACCTTTGCAAAATTCCTTTCCCTCCCGACAG
-------> IS1106
3110
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3160
AATACCCCCTTAATCCTCCCCGATACCCGATAATCAGGCATCCGGCGCCTTTAGGCGGCA
3210
GCGGGCGCACTTAACCTGTTGGCGGCTTTCAAAAGGTTCAAACACATCGCCTTCAGGTGC
3260
CTTTGCGCACTCACTTTAATCAGTCCGAAATAGGCCGCCCGCGCATAGCAGAACTTACGG
3310
TGCAGCGTACCGAAGCTT
HindIII

Figure 3

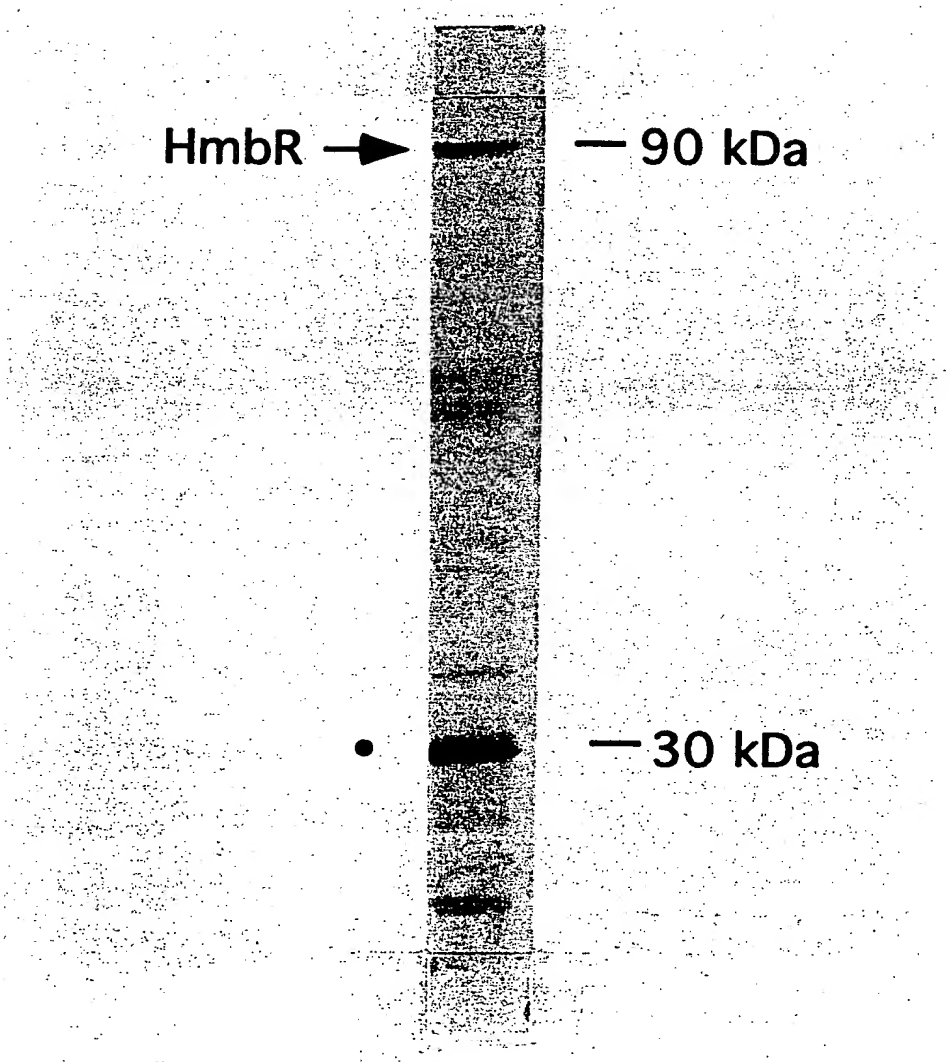

FIG. 4A


```
TBP1M    MQQQHLFRLNILCLSLMTALPVYA---ENVQAEQAQEKQLDTIOVKAKKQ   47
LBPA     MNKKHGFQLTLTALAVAAAFPSYAANPETAAPDAAQTQSLKEVTVRAAKV   50
HMBR     MKPLQMLPIAALVGSIFGN-PVFAADEAATETTPVKAE------VKAVR    43
         *.  . ....   .. .. * .*  ..........     *.*  .

TBP1M    KTRRDNEVTGLGKLVKSSDTLSKEQVLNIRDLTRYDPGIAVVEQQGRGASS  97
LBPA     -GRRSKEATGLGKIAKTSETLNKEQVLGIRDLTRYDPGVAVVEQQGNGASG  99
HMBR     KGQRNA-PAAVERV--NLNRIKQEMIRDNKDLVRYSTDVGLSDSGRHQK-   89
           ..*.   ..... . . ...* . . .**.**..... . *. ..

TBP1M    GYSIRGMDKNRVSLTVDGVSQIQSYTAQAALGGTRTAGSSGAINEIEYEN  147
LBPA     GYSIRGVDKNRVAVSVDGVAQIQAFTVQGSLSGYGGRGGSGAINEIEYEN  149
HMBR     GFAVRGVEGNRVGVSIDGVNLPDS--EENSLYARYGNFNSSRLS-IDPEL  136
         *...**.. ***....***.  ..   ...* .  .   .*. .. *. *

TBP1M    VKAVEISKGSNSSEYGNGALAGSVAFQTKTAADIIGEGKQWGIQSKTAYS  197
LBPA     ISTVEIDKGAGSSDHGSGALGGAVAFRTKEAADLISDGKSWGIQAKTAYG  199
HMBR     VRNIDIVKGADSFNTGSGALGGGVYNQTLQGRDLLLPERQFGVMMKNGYS  186
         .....* **..*  .  *.***.*.*...*   . *..  .. .*.  *..*.

TBP1M    GKDHALTQSLALAGRSGGAEALLIYTKRRGREIHAHKDAGKGVQ-SFNRL  246
LBPA     SKNRQFMKSLGAGFSKDGWEGLLIRTERQGRETHPHGDIADGVAYGINRL  249
HMBR     TRNREWTNTLGFGVSNDRVDAALLYSQRRGHETESAG------------  223
         .....  ..*. . ...  .. *. ..*.*.*...
```

FIG. 4B


```
TBP1M    PICRFGNNTYT-DCTPRNIGGNGYYAAVQDNVRLGRWADVGAGIRYDYRS   601
LBPA     SVCGYIETLRSRKCVPRKINGSNIHISLNDRFSIGKYFDFSLGGRYDRKN   635
HMBR     -----------SSIQHPVKTTNYGFSLSDQIQWNDVFSSRAGIRYDHTK   460
                    . . . . . . . . . . * . . . . * *** .

TBP1M    THSED--------KSVSTGTHRNLSWNAGVVLKP--FTWMDLTYRASTGF   641
LBPA     FTTSE--------ELVRSGRYVDRSWNSGIVFKP--NRHFSLSYRASSGF   675
HMBR     MTPQELNAECHACDKTPPAANTYKGWSGFVGLAAQLNQAWRVGYDITSGY   510
           . .          . . . .     .*. . . .       . .*  . .*.

TBP1M    RLPSFAEMYGWRA----GESLKTLDLKPEKSFNREAGIVFKGDFGNLEAS   687
LBPA     RTPSFQELFGIDIYHDYPKGWQRPALKSEKAANREIGLQWKGDFGFLEIS   725
HMBR     RVPNASEVY-FTYNHGSGNWLPNPNLKAERTTTHTLSLQGRSEKGTLDAN   559
         * *.  *. .          .     .**.*. . . . . .  . . * *. .

TBP1M    YFNNAYRDLIAFGYET---RTQNGQTSASGDPGYR---------------   719
LBPA     SFRNRYTDMIAVADHKTKLPNQAGQLTEIDIRDYY---------------   760
HMBR     LYQSNYRNFLS---EEQKLTT-SGDVSCTQMNYYYGMCSNPYSEKLEWQM   605
           . . . *  . . . .    . .     . .*. .        *

TBP1M    -NAQNARIAGINILGKIDWHGVWGGLPDG--LYSTLAYNRIKVKDADIRA   766
LBPA     -NAQNMSLQGVNILGKIDWNGVYGKLPEG--LYTTLAYNRIKPKSVSNRP   807
HMBR     QNIDKARIRGIELTGRLNVDKVASFVPEGWKLFGSLGYAKSKLSG-----   650
           . . . .  *. . .  *. . .  . *  . . *.*   *. . .*.*. .  *  . .
```

FIG. 4C


```
TBP1M    DRTFVTSYLFDAVQPSRYVLGLGYDHPDGIWGINTMFTYSKAKSVDE---   813
LBPA     GLSL-RSYALDAVQPSRYVLGFGYDQPEGKWGANIMLTYSKGKNPDE---   853
HMBR     DNSLLST------QPLKVIAGIDYESPSEKWGVFSRLTYLGAKKVKDAQY   694
                      **  .  . *.*. *.. **    ..**  .*.  ..

TBP1M    -LLGSQALLNGNANAKKAASRRTRPWYVTDVSGYYNIKKHLTLRAGVYNL   862
LBPA     -L----AYLAGDQK-RYSTKRASSSWSTADVSAYLNLKKRLTLRAAIYNI   897
HMBR     TVYENKGWGTPLQKKVKDYPWLNKSAYVFDMYGFYKPVKNLTLRAGVYNV   744
           .    .   .  ..   .  . ...  . *. . .  *.*****..**.

TBP1M    LNYRYVTWENVRQ--TAGGAVNQHKNVGVYNRYAAPGRNYTFSLEMKF    908
LBPA     GNYRYVTWESLRQ--TAESTANRHGGDSNYGRYAAPGRNFSLALEMKF    943
HMBR     FNRKYTTWDSLRGLYSYSTTNSVDRDGKGLDRYRAPSRNYAVSLEWKF    792
           *  .*.*...*     . ... .  .  .  .  .**  **.**.. .**  **
```

Figure 5

SHEET 14/47

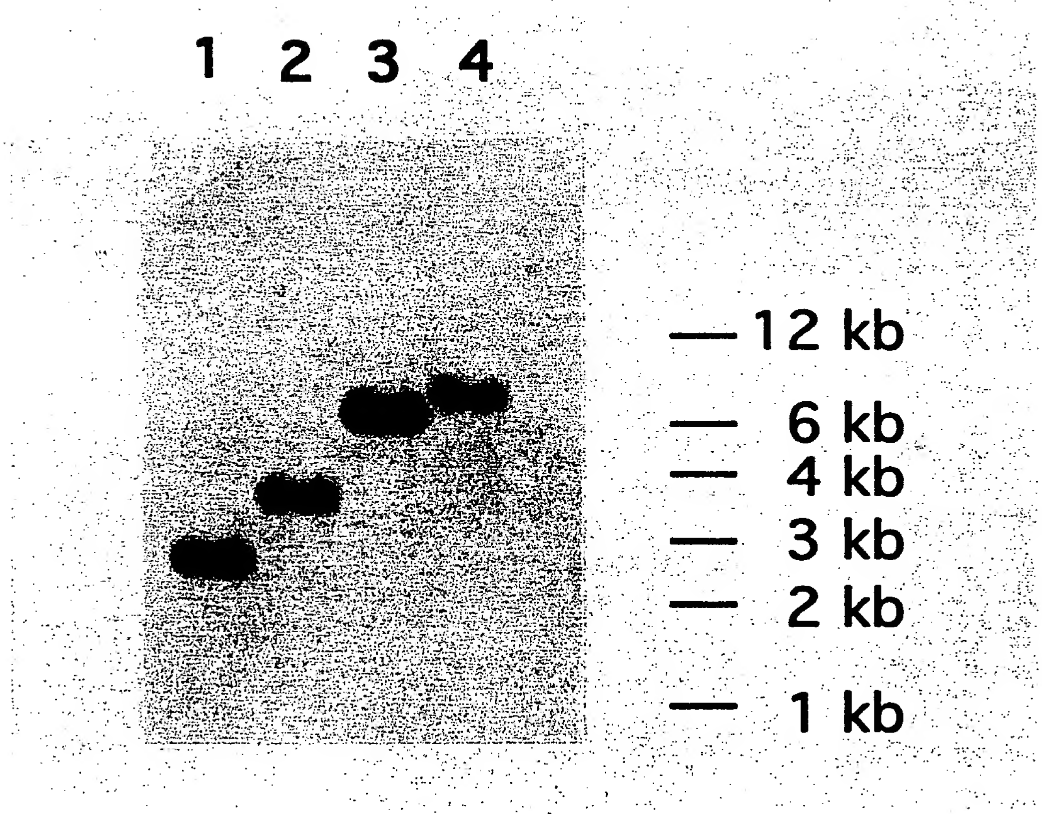

FIG. 6

SHEET 15/47

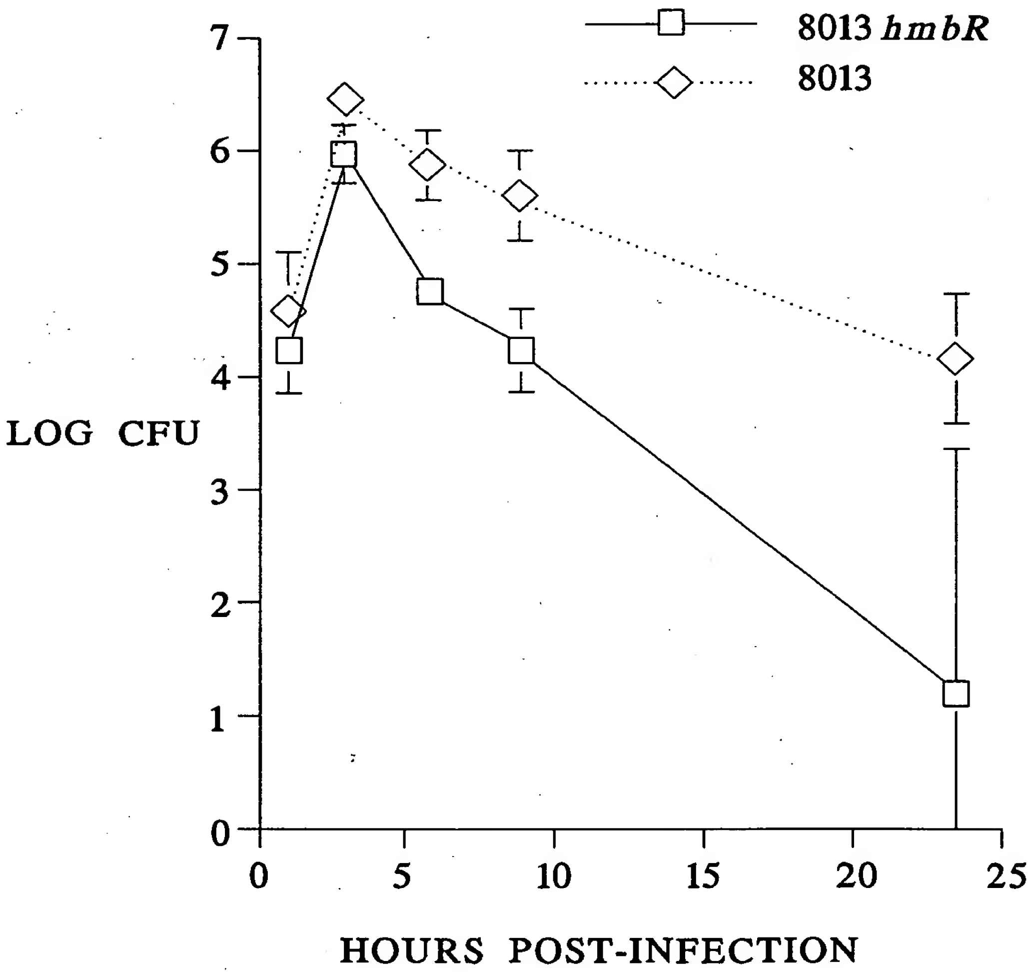

FIG. 7A


```
ATG AAA CCA TTA CAA ATG CCC CCT ATC GCC GCG CTG CTC GGC AGT ATT      48
Met Lys Pro Leu Gln Met Pro Pro Ile Ala Ala Leu Leu Gly Ser Ile
 1               5                  10                  15

TTC GGC AAT CCG GTC TTT GCG GCA GAT GAA GCT GCA ACT GAA ACC ACA      96
Phe Gly Asn Pro Val Phe Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr
            20                  25                  30

CCC GTT AAG GCA GAG GTA AAA GCA GTG CGC GTT AAA GGT CAG CGC AAT     144
Pro Val Lys Ala Glu Val Lys Ala Val Arg Val Lys Gly Gln Arg Asn
        35                  40                  45

GCG CCT GCG GCT GTG GAA CGC GTC AAC CTT AAC CGT ATC AAA CAA GAA     192
Ala Pro Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile Lys Gln Glu
    50                  55                  60

ATG ATA CGC GAC AAT AAA GAC TTG GTG CGC TAT TCC ACC GAT GTC GGC     240
Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly
65                  70                  75                  80

TTG AGC GAC AGG AGC CGT CAT CAA AAA GGC TTT GCC ATT CGC GGC GTG     288
Leu Ser Asp Arg Ser Arg His Gln Lys Gly Phe Ala Ile Arg Gly Val
                85                  90                  95
```

FIG. 7B


```
GAA GGC GAC CGT GTC GGC GTT AGT ATT GAC GGC GTA AAC CTG CCT GAT      336
Glu Gly Asp Arg Val Gly Val Ser Ile Asp Gly Val Asn Leu Pro Asp
            100                 105                 110

TCC GAA GAA AAC TCG CTG TAC GCC CGT TAT GGC AAC TTC AAC AGC TCG      384
Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser
        115                 120                 125

CGT CTG TCT ATC GAC CCC GAA CTC GTG CGC AAC ATC GAC ATC GTA AAA      432
Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Asp Ile Val Lys
    130                 135                 140

GGG GCG GAC TCT TTC AAT ACC GGC AGC GGC GCC TTG GGC GGC GGT GTG      480
Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Gly Val
145                 150                 155                 160

AAT TAC CAA ACC CTG CAA GGA CGT GAC TTA CTG TTG CCT GAA CGG CAG      528
Asn Tyr Gln Thr Leu Gln Gly Arg Asp Leu Leu Leu Pro Glu Arg Gln
                165                 170                 175

TTC GGC GTG ATG ATG AAA AAC GGT TAC AGC ACG CGT AAC CGT GAA TGG      576
Phe Gly Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp
            180                 185                 190
```

FIG. 7C


```
ACA AAT ACC CTC GGT TTC GGC GTG AGC AAC GAC CGC GTG GAT GCC GCT      624
Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala
        195                 200                 205

TTG CTG TAT TCG CAA CGG CGC GGC CAT GAA ACT GAA AGC GCG GGC AAG      672
Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Lys
    210                 215                 220

CGT GGT TAT CCG GTA GAG GGT GCT GGT AGC GGA GCG AAT ATC CGT GGT      720
Arg Gly Tyr Pro Val Glu Gly Ala Gly Ser Gly Ala Asn Ile Arg Gly
225                 230                 235                 240

TCT GCG CGC GGT ATT CCT GAT CCG TCC CAA CAC AAA TAC CAC AGC TTC      768
Ser Ala Arg Gly Ile Pro Asp Pro Ser Gln His Lys Tyr His Ser Phe
                245                 250                 255

TTG GGT AAG ATT GCT TAT CAA ATC AAC GAC AAC CAC CGC ATC GGC GCA      816
Leu Gly Lys Ile Ala Tyr Gln Ile Asn Asp Asn His Arg Ile Gly Ala
            260                 265                 270

TCG CTC AAC GGT CAG CAG GGG CAT AAT TAC ACG GTT GAA GAG TCT TAC      864
Ser Leu Asn Gly Gln Gln Gly His Asn Tyr Thr Val Glu Glu Ser Tyr
        275                 280                 285
```

FIG. 7D

```
AAC CTG CTT GCT TCT TAT TGG CGT GAA GCT GAC GAT GTC AAC AGA CGG      912
Asn Leu Leu Ala Ser Tyr Trp Arg Glu Ala Asp Asp Val Asn Arg Arg
    290                 295                 300

CGT AAC ACC AAC CTC TTT TAC GAA TGG ACG CCG GAA TCC GAC CGG TTG      960
Arg Asn Thr Asn Leu Phe Tyr Glu Trp Thr Pro Glu Ser Asp Arg Leu
305                 310                 315                 320

TCT ATG GTA AAA GCG GAT GTC GAT TAT CAA AAA ACC AAA GTA TCT GCG     1008
Ser Met Val Lys Ala Asp Val Asp Tyr Gln Lys Thr Lys Val Ser Ala
                325                 330                 335

GTC AAC TAC AAA GGT TCG TTC CCG ACG AAT TAC ACC ACA TGG GAA ACC     1056
Val Asn Tyr Lys Gly Ser Phe Pro Thr Asn Tyr Thr Thr Trp Glu Thr
            340                 345                 350

GAG TAC CAT AAA AAG GAA GTT GGC GAA ATC TAT AAC CGC AGC ATG GAT     1104
Glu Tyr His Lys Lys Glu Val Gly Glu Ile Tyr Asn Arg Ser Met Asp
        355                 360                 365

ACA ACC TTC AAA CGT ATT ACG CTG CGT ATG GAC AGC CAT CCG TTG CAA     1152
Thr Thr Phe Lys Arg Ile Thr Leu Arg Met Asp Ser His Pro Leu Gln
    370                 375                 380
```

FIG. 7E

```
CTC GGG GGG GGG CGA CAC CGC CTG TCG TTC AAA ACC TTT GCC GGG CAG      1200
Leu Gly Gly Gly Arg His Arg Leu Ser Phe Lys Thr Phe Ala Gly Gln
385                 390                 395                 400

CGT GAT TTT GAA AAC TTA AAC CGC GAC GAT TAC TAC TTC AGC GGC CGT      1248
Arg Asp Phe Glu Asn Leu Asn Arg Asp Asp Tyr Tyr Phe Ser Gly Arg
                405                 410                 415

GTT GTT CGA ACC ACC AAC AGT ATC CAG CAT CCG GTG AAA ACC ACC AAC      1296
Val Val Arg Thr Thr Asn Ser Ile Gln His Pro Val Lys Thr Thr Asn
            420                 425                 430

TAC GGT TTC TCG CTG TCC GAC CAA ATC CAA TGG AAC GAC GTG TTC AGT      1344
Tyr Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe Ser
        435                 440                 445

AGC CGC GCA GGT ATC CGT TAC GAC CAC ACC AAA ATG ACG CCT CAG GAA      1392
Ser Arg Ala Gly Ile Arg Tyr Asp His Thr Lys Met Thr Pro Gln Glu
    450                 455                 460

TTG AAT GCC GAC TGT CAT GCT TGT GAC AAA ACA CCG CCT GCA GCC AAC      1440
Leu Asn Ala Asp Cys His Ala Cys Asp Lys Thr Pro Pro Ala Ala Asn
465                 470                 475                 480
```

FIG. 7F

```
ACT TAT AAA GGC TGG AGC GGA TTT GTC GGC TTG GCG GCG CAG CTG AGC      1488
Thr Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu Ser
                485                 490                 495

CAA ACA TGG CGT TTG GGT TAC GAT GTG ACC TCA GGT TTC CGC GTG CCG      1536
Gln Thr Trp Arg Leu Gly Tyr Asp Val Thr Ser Gly Phe Arg Val Pro
            500                 505                 510

AAT GCG TCT GAA GTG TAT TTC ACT TAC AAC CAC GGT TCG GGC ACT TGG      1584
Asn Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Thr Trp
        515                 520                 525

AAG CCT AAT CCT AAT TTG AAG GCA GAA CGC AGC ACC ACC CAC ACC CTG      1632
Lys Pro Asn Pro Asn Leu Lys Ala Glu Arg Ser Thr Thr His Thr Leu
    530                 535                 540

TCC TTG CAG GGG CGC GGC GAC AAA GGG ACA CTG GAT GCC AAC CTG TAT      1680
Ser Leu Gln Gly Arg Gly Asp Lys Gly Thr Leu Asp Ala Asn Leu Tyr
545                 550                 555                 560

CAA AGC AAT TAC CGA AAC TTC CTG TCG GAA GAG CAG AAT CTG ACT GTC      1728
Gln Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Asn Leu Thr Val
                565                 570                 575
```

FIG. 7G

```
AGC GGC ACA CCC GGC TGT ACT GAG GAG GAT GCT TAC TAC TAT AGA TGC      1776
Ser Gly Thr Pro Gly Cys Thr Glu Glu Asp Ala Tyr Tyr Tyr Arg Cys
            580                 585                 590

AGC GAC CCC TAC AAA GAA AAA CTG GAT TGG CAG ATG AAA AAT ATC GAC      1824
Ser Asp Pro Tyr Lys Glu Lys Leu Asp Trp Gln Met Lys Asn Ile Asp
        595                 600                 605

AAG GCC AGA ATC CGC GGT ATC GAG TTG ACA GGC CGT CTG AAT GTG GAC      1872
Lys Ala Arg Ile Arg Gly Ile Glu Leu Thr Gly Arg Leu Asn Val Asp
    610                 615                 620

AAA GTA GCG TCT TTT GTT CCT GAG GGT TGG AAA CTG TTC GGC TCG CTG      1920
Lys Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser Leu
625                 630                 635                 640

GGT TAT GCG AAA AGC AAA CTG TCG GGC GAC AAC AGC CTG CTG TCC ACA      1968
Gly Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Ser Thr
                645                 650                 655

CAG CCG CTG AAA GTG ATT GCC GGT ATC GAC TAT GAA AGT CCG AGC GAA      2016
Gln Pro Leu Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser Glu
            660                 665                 670
```

FIG. 7H


```
AAA TGG GGC GTA TTC TCC CGC CTG ACC TAT CTA GGC GCG AAA AAG GTC      2064
Lys Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys Val
        675                 680                 685

AAA GAC GCG CAA TAC ACC GTT TAT GAA AAC AAG GGC TGG GGT ACG CCT      2112
Lys Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Trp Gly Thr Pro
    690                 695                 700

TTG CAG AAA AAG GTA AAA GAT TAC CCG TGG CTG AAC AAG TCG GCT TAT      2160
Leu Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala Tyr
705                 710                 715                 720

GTG TTT GAT ATG TAC GGC TTC TAC AAA CCG GCT AAA AAC CTG ACT TTG      2208
Val Phe Asp Met Tyr Gly Phe Tyr Lys Pro Ala Lys Asn Leu Thr Leu
                725                 730                 735

CGT GCA GGC GTG TAC AAC CTG TTC AAC CGC AAA TAC ACC ACT TGG GAT      2256
Arg Ala Gly Val Tyr Asn Leu Phe Asn Arg Lys Tyr Thr Thr Trp Asp
            740                 745                 750

TCC CTG CGC GGT TTA TAT AGC TAC AGC ACC ACC AAT GCG GTC GAC CGC      2204
Ser Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ala val Asp Arg
        755                 760                 765
```

FIG. 7I


```
GAT GGC AAA GGC TTA GAC CGC TAC CGC GCC CCA GGC CGC AAT TAC GCC      2352
Asp Gly Lys Gly Leu Asp Arg Tyr Arg Ala Pro Gly Arg Asn Tyr Ala
    770                 775                 780

GTA TCG CTG GAA TGG AAG TTT TAA                                    2375
Val Ser Leu Glu Trp Lys Phe  *
785                 790
```

FIG. 8A

```
ATG AAA CCA TTA CAA ATG CTC CCT ATC GCC GCG CTG GTC GGC AGT ATT      48
Met Lys Pro Leu Gln Met Leu Pro Ile Ala Ala Leu Val Gly Ser Ile
 1               5                  10                  15

TTC GGC AAT CCG GTC TTT GCG GCA GAT GAA GCT GCA ACT GAA ACC ACA      96
Phe Gly Asn Pro Val Phe Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr
            20                  25                  30

CCC GTT AAG GCA GAG GTA AAA GCA GTG CGC GTT AAA GGC CAG CGC AAT     144
Pro Val Lys Ala Glu Val Lys Ala Val Arg Val Lys Gly Gln Arg Asn
        35                  40                  45

GCG CCT GCG GCT GTG GAA CGC GTC AAC CTT AAC CGT ATC AAA CAA GAA     192
Ala Pro Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile Lys Gln Glu
    50                  55                  60

ATG ATA CGC GAC AAC AAA GAC TTG GTG CGC TAT TCC ACC GAT GTC GGC     240
Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly
65                  70                  75                  80

TTG AGC GAC AGC GGC CGC CAT CAA AAA GGC TTT GCT GTT CGC GGC GTG     288
Leu Ser Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val Arg Gly Val
                85                  90                  95
```

FIG. 8B

```
GAA GGC AAC CGT GTC GGC GTG AGC ATA GAC GGC GTA AAC CTG CCT GAT      336
Glu Gly Asn Arg Val Gly Val Ser Ile Asp Gly Val Asn Leu Pro Asp
            100                 105                 110

TCC GAA GAA AAC TCG CTG TAC GCC CGT TAT GGC AAC TTC AAC AGC TCG      384
Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser
        115                 120                 125

CGT CTG TCT ATC GAC CCC GAA CTC GTG CGC AAC ATC GAC ATC GTA AAA      432
Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Asp Ile Val Lys
    130                 135                 140

GGG GCG GAC TCT TTC AAT ACC GGC AGC GGC GCC TTG GGC GGC GGT GTG      480
Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Gly Val
145                 150                 155                 160

AAT TAC CAA ACC CTG CAA GGA CGT GAC TTA CTG TTG CCT GAA CGG CAG      528
Asn Tyr Gln Thr Leu Gln Gly Arg Asp Leu Leu Leu Pro Glu Arg Gln
                165                 170                 175

TTC GGC GTG ATG ATG AAA AAC GGT TAC AGC ACG CGT AAC CGT GAA TGG      576
Phe Gly Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp
            180                 185                 190
```

FIG. 8C

```
ACA AAT ACC CTC GGT TTC GGC GTG AGC AAC GAC CGC GTG GAT GCC GCT      624
Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala
        195                 200                 205

TTG CTG TAT TCG CAA CGG CGC GGC CAT GAA ACT GAA AGC GCG GGC AAG      672
Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Lys
    210                 215                 220

CGT GGT TAT CCG GTA GAG GGT GCT GGT AGC GGA GCG AAT ATC CGT GGT      720
Arg Gly Tyr Pro Val Glu Gly Ala Gly Ser Gly Ala Asn Ile Arg Gly
225                 230                 235                 240

TCT GCG CGC GGT ATT CCT GAT CCG TCC CAA CAC AAA TAC CAC AGC TTC      768
Ser Ala Arg Gly Ile Pro Asp Pro Ser Gln His Lys Tyr His Ser Phe
                245                 250                 255

TTG GGT AAG ATT GCT TAT CAA ATC AAC GAC AAC CAC CGC ATC GGC GCA      816
Leu Gly Lys Ile Ala Tyr Gln Ile Asn Asp Asn His Arg Ile Gly Ala
            260                 265                 270

TCG CTC AAC GGT CAG CAG GGG CAT AAT TAC ACG GTT GAA GAG TCT TAC      864
Ser Leu Asn Gly Gln Gln Gly His Asn Tyr Thr Val Glu Glu Ser Tyr
        275                 280                 285
```

FIG. 8D

```
AAC CTG CTT GCT TCT TAT TGG CGT GAA GCT GAC GAT GTC AAC AGA CGG      911
Asn Leu Leu Ala Ser Tyr Trp Arg Glu Ala Asp Asp Val Asn Arg Arg
    290                 295                 300

CGT AAC ACC AAC CTC TTT TAC GAA TGG ACG CCG GAA TCC GAC CGG TTG      960
Arg Asn Thr Asn Leu Phe Tyr Glu Trp Thr Pro Glu Ser Asp Arg Leu
305                 310                 315                 320

TCT ATG GTA AAA GCG GAT GTC GAT TAT CAA AAA ACC AAA GTA TCT GCG     1008
Ser Met Val Lys Ala Asp Val Asp Tyr Gln Lys Thr Lys Val Ser Ala
                325                 330                 335

GTC AAC TAC AAA GGT TCG TTC CCG ATA GAG GAT TCT TCC ACC TTG ACA     1056
Val Asn Tyr Lys Gly Ser Phe Pro Ile Glu Asp Ser Ser Thr Leu Thr
            340                 345                 350

CGT AAC TAC AAT CAA AAG GAC TTG GAT GAA ATC TAC AAC CGC AGT ATG     1104
Arg Asn Tyr Asn Gln Lys Asp Leu Asp Glu Ile Tyr Asn Arg Ser Met
        355                 360                 365

GAT ACC CGC TTC AAA CGC ATT ACC CTG CGT TTG GAC AGC CAT CCG TTG     1152
Asp Thr Arg Phe Lys Arg Ile Thr Leu Arg Leu Asp Ser His Pro Leu
    370                 375                 380
```

FIG. 8E


```
CAA CTC GGG GGG GGG CGA CAC CGC CTG TCG TTT AAA ACT TTC GCC AGC      1200
Gln Leu Gly Gly Gly Arg His Arg Leu Ser Phe Lys Thr Phe Ala Ser
385                 390                 395                 400

CGC CGT GAT TTT GAA AAC CTA AAC CGC GAC GAT TAT TAC TTC AGC GGC      1248
Arg Arg Asp Phe Glu Asn Leu Asn Arg Asp Asp Tyr Tyr Phe Ser Gly
                405                 410                 415

CGT GTT GTT CGA ACC ACC AGC AGT ATC CAG CAT CCG GTG AAA ACC ACC      1296
Arg Val Val Arg Thr Thr Ser Ser Ile Gln His Pro Val Lys Thr Thr
            420                 425                 430

AAC TAC GGT TTC TCA CTG TCT GAC CAA ATT CAA TGG AAC GAC GTG TTC      1344
Asn Tyr Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe
        435                 440                 445

AGT AGC CGC GCA GGT ATC CGT TAC GAT CAT ACC AAA ATG ACG CCT CAG      1392
Ser Ser Arg Ala Gly Ile Arg Tyr Asp His Thr Lys Met Thr Pro Gln
    450                 455                 460

GAA TTG AAT GCC GAG TGT CAT GCT TGT GAC AAA ACA CCG CCT GCA GCC      1440
Glu Leu Asn Ala Glu Cys His Ala Cys Asp Lys Thr Pro Pro Ala Ala
465                 470                 475                 480
```

FIG. 8F


```
AAC ACT TAT AAA GGC TGG AGC GGT TTT GTC GGC TTG GCG GCG CAA CTG      1488
Asn Thr Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu
                485                 490                 495

AAT CAG GCT TGG CGT GTC GGT TAC GAC ATT ACT TCC GGC TAC CGT GTC      1536
Asn Gln Ala Trp Arg Val Gly Tyr Asp Ile Thr Ser Gly Tyr Arg Val
            500                 505                 510

CCC AAT GCG TCC GAA GTG TAT TTC ACT TAC AAC CAC GGT TCG GGT AAT      1584
Pro Asn Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Asn
        515                 520                 525

TGG CTG CCC AAT CCC AAC CTG AAA GCC GAG CGC ACG ACC ACC CAC ACC      1632
Trp Leu Pro Asn Pro Asn Leu Lys Ala Glu Arg Thr Thr Thr His Thr
    530                 535                 540

CTC TCT CTG CAA GGC CGC AGC GAA AAA GGT ACT TTG GAT GCC AAC CTG      1680
Leu Ser Leu Gln Gly Arg Ser Glu Lys Gly Thr Leu Asp Ala Asn Leu
545                 550                 555                 560

TAT CAA AGC AAT TAC CGC AAT TTC CTG TCT GAA GAG CAG AAG CTG ACC      1728
Tyr Gln Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Lys Leu Thr
                565                 570                 575
```

FIG. 8G


```
ACC AGC GGC GAT GTC AGC TGT ACT CAG ATG AAT TAC TAC TAC GGT ATG      1776
Thr Ser Gly Asp Val Ser Cys Thr Gln Met Asn Tyr Tyr Tyr Gly Met
            580                 585                 590

TGT AGC AAT CCT TAT TCC GAA AAA CTG GAA TGG CAG ATG CAA AAT ATC      1824
Cys Ser Asn Pro Tyr Ser Glu Lys Leu Glu Trp Gln Met Gln Asn Ile
        595                 600                 605

GAC AAG GCC AGA ATC CGC GGT ATC GAG CTG ACG GGC CGT CTG AAT GTG      1872
Asp Lys Ala Arg Ile Arg Gly Ile Glu Leu Thr Gly Arg Leu Asn Val
    610                 615                 620

GAC AAA GTA GCG TCT TTT GTT CCT GAG GGC TGG AAA CTG TTC GGC TCG      1920
Asp Lys Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser
625                 630                 635                 640

CTG GGT TAT GCG AAA AGC AAA CTG TCG GGC GAC AAC AGC CTG CTG TCC      1968
Leu Gly Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Ser
                645                 650                 655

ACC CAG CCG TTG AAA GTG ATT GCC GGT ATC GAC TAT GAA AGT CCG AGC      2016
Thr Gln Pro Leu Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser
            660                 665                 670
```

FIG. 8H


```
GAA AAA TGG GGC GTG TTC TCC CGC CTG ACC TAT CTG GGC GCG AAA AAG      2064
Glu Lys Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys
        675                 680                 685

GTC AAA GAC GCG CAA TAC ACC GTT TAT GAA AAC AAG GGC TGG GGT ACG      2112
Val Lys Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Trp Gly Thr
    690                 695                 700

CCT TTG CAG AAA AAG GTA AAA GAT TAC CCG TGG CTG AAC AAG TCG GCT      2160
Pro Leu Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala
705                 710                 715                 720

TAT GTG TTC GAT ATG TAC GGC TTC TAC AAA CCG GTG AAA AAC CTG ACT      2208
Tyr Val Phe Asp Met Tyr Gly Phe Tyr Lys Pro Val Lys Asn Leu Thr
                725                 730                 735

TTG CGT GCA GGC GTA TAT AAT GTG TTC AAC CGC AAA TAC ACC ACT TGG      2256
Leu Arg Ala Gly Val Tyr Asn Val Phe Asn Arg Lys Tyr Thr Thr Trp
            740                 745                 750

GAT TCC CTG CGC GGC CTG TAT AGC TAC AGC ACC ACC AAC TCG GTC GAC      2304
Asp Ser Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ser Val Asp
        755                 760                 765
```

FIG. 8I


```
CGC GAT GGC AAA GGC TTA GAC CGC TAC CGC GCC CCA AGC CGT AAT TAC      2352
Arg Asp Gly Lys Gly Leu Asp Arg Tyr Arg Ala Pro Ser Arg Asn Tyr
    770                 775                 780

GCC GTA TCG CTG GAA TGG AAG TTT TAA                                 2379
Ala Val Ser Leu Glu Trp Lys Phe  *
785                 790
```

FIG. 9A

```
ATG AAA CCA TTA CAC ATG CTT CCT ATT GCC GCG CTG GTC GGC AGT ATT      48
Met Lys Pro Leu His Met Leu Pro Ile Ala Ala Leu Val Gly Ser Ile
 1               5                  10                  15

TTC GGC AAT CCG GTC TTG GCA GCG GAT GAA GCT GCA ACC GAA ACC ACA      96
Phe Gly Asn Pro Val Leu Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr
            20                  25                  30

CCC GTT AAA GCA GAG ATA AAA GAA GTG CGC GTT AAA GAC CAG CTT AAT     144
Pro Val Lys Ala Glu Ile Lys Glu Val Arg Val Lys Asp Gln Leu Asn
        35                  40                  45

GCG CCT GCA ACC GTG GAA CGT GTC AAC CTC GGC CGC ATT CAA CAG GAA     192
Ala Pro Ala Thr Val Glu Arg Val Asn Leu Gly Arg Ile Gln Gln Glu
    50                  55                  60

ATG ATA CGC GAC AAC AAA GAC TTG GTG CGT TAC TCC ACC GAC GTC GGC     240
Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly
65                  70                  75                  80

TTG AGC GAT AGC GGC CGC CAT CAA AAA GGC TTT GCT GTG CGC GGC GTG     288
Leu Ser Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val Arg Gly Val
                85                  90                  95
```

FIG. 9B


```
GAA GGC AAC CGT GTC GGT GTC AGC ATT GAC GGC GTG AGC CTG CCT GAT      336
Glu Gly Asn Arg Val Gly Val Ser Ile Asp Gly Val Ser Leu Pro Asp
            100                 105                 110

TCG GAA GAA AAC TCA CTG TAT GCA CGT TAT GGC AAC TTC AAC AGC TCG      384
Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser
        115                 120                 125

CGC CTG TCT ATC GkC CCC GAA CTC GTG CGC AAC ATC GAA ATC GCG AAG      432
Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Glu Ile Ala Lys
    130                 135                 140

GGC GCT GAC TCT TTC AAT ACC GGT AGC GGC GCA TTG GGT GGC GGC GTG      480
Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Gly Val
145                 150                 155                 160

AAT TAC CAA ACC CTG CAA GGA CAT GAT TTG CTG TTG GAC GAC AGG CAA      528
Asn Tyr Gln Thr Leu Gln Gly His Asp Leu Leu Leu Asp Asp Arg Gln
                165                 170                 175

TTC GGC GTG ATG ATG AAA AAC GGT TAC AGC AGC CGC AAC CGC GAA TGG      576
Phe Gly Val Met Met Lys Asn Gly Tyr Ser Ser Arg Asn Arg Glu Trp
            180                 185                 190
```

FIG. 9C

```
ACA AAT ACA CTC GGT TTC GGT GTG AGC AAC GAC CGC GTG GAT GCC GCT      624
Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala
        195                 200                 205

TTG CTG TAT TCG CAA CGT CGC GGT CAT GAG ACC GAA AGC GCG GGC GAG      672
Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Glu
    210                 215                 220

CGT GGC TAT CCG GTA GAG GGT GCT GGC AGC GGA GCA ATT ATC CGT GGT      720
Arg Gly Tyr Pro Val Glu Gly Ala Gly Ser Gly Ala Ile Ile Arg Gly
225                 230                 235                 240

TCG TCA CGC GGT ATC CCT GAT CCG TCC AAA CAC AAA TAC CAC AAC TTC      768
Ser Ser Arg Gly Ile Pro Asp Pro Ser Lys His Lys Tyr His Asn Phe
                245                 250                 255

TTG GGT AAG ATT GCT TAT CAA ATC AAC GAC AAG CAC CGC ATC GGC CCA      816
Leu Gly Lys Ile Ala Tyr Gln Ile Asn Asp Lys His Arg Ile Gly Pro
            260                 265                 270

TCG TTT AAC GGC CAG CAG GGG CAT AAT TAC ACG ATT GAA GAG TCT TAT      864
Ser Phe Asn Gly Gln Gln Gly His Asn Tyr Thr Ile Glu Glu Ser Tyr
        275                 280                 285
```

FIG. 9D

```
AAC CTG ACC GCT TCT TCC TGG CGC GAA GCC GAT GAC GTA AAC AGA CGG      912
Asn Leu Thr Ala Ser Ser Trp Arg Glu Ala Asp Asp Val Asn Arg Arg
    290                 295                 300

CGC AAT GCC AAC CTC TTT TAC GAA TGG ACG CCT GAT TCA AAT TGG CTG      960
Arg Asn Ala Asn Leu Phe Tyr Glu Trp Thr Pro Asp Ser Asn Trp Leu
305                 310                 315                 320

TCG TCT TTG AAG GCG GAC TTC GAT TAT CAG ACA ACC AAA GTG GCG GCG     1008
Ser Ser Leu Lys Ala Asp Phe Asp Tyr Gln Thr Thr Lys Val Ala Ala
                325                 330                 335

GTT AAC AAC AAA GGC TCG TTC CCG ACG GAT TAT TCC ACC TGG ACG CGC     1056
Val Asn Asn Lys Gly Ser Phe Pro Thr Asp Tyr Ser Thr Trp Thr Arg
            340                 345                 350

AAC TAT AAT CAG AAG GAT TTG GAG AAT ATA TAC AAC CGC AGC ATG GAC     1104
Asn Tyr Asn Gln Lys Asp Leu Glu Asn Ile Tyr Asn Arg Ser Met Asp
        355                 360                 365

ACC CGA TTC AAA CGT TTT ACT TTG CGT ATG GAC AGC CAA CCG TTG CAA     1152
Thr Arg Phe Lys Arg Phe Thr Leu Arg Met Asp Ser Gln Pro Leu Gln
    370                 375                 380
```

FIG. 9E

```
CTG GGC GGC CAA CAT CGC TTG TCG CTT AAA ACT TTC GCC AGT CGG CGT      1200
Leu Gly Gly Gln Hls Arg Leu Ser Leu Lys Thr Phe Ala Ser Arg Arg
385                 390                 395                 400

GAG TTT GAA AAC TTA AAC CGC GAC GAT TAT TAC TTC AGC GAA AGA GTA      1248
Glu Phe Glu Asn Leu Asn Arg Asp Asp Tyr Tyr Phe Ser Glu Arg Val
                405                 410                 415

TCC CGT ACT ACC AGC TCG ATT CAA CAC CCC GTG AAA ACC ACT AAT TAT      1296
Ser Arg Thr Thr Ser Ser Ile Gln His Pro Val Lys Thr Thr Asn Tyr
            420                 425                 430

GGT TTC TCA CTG TCT GAT CAA ATC CAA TGG AAC GAC GTG TTC AGC AGC      1344
Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe Ser Ser
        435                 440                 445

CGT GCA GAT ATC CGT TAC GAT CAT ACC AAA ATG ACG CCT CAG GAA TTG      1392
Arg Ala Asp Ile Arg Tyr Asp His Thr Lys Met Thr Pro Gln Glu Leu
    450                 455                 460

AAT GCC GAG TGT CAT GCT TGT GAC AAA ACA CCG CCT GCA GCC AAT ACT      1440
Asn Ala Glu Cys His Ala Cys Asp Lys Thr Pro Pro Ala Ala Asn Thr
465                 470                 475                 480
```

FIG. 9F

```
TAT AAA GGC TGG AGC GGA TTT GTC GGT TTG GCG GCG CAA CTG AAT CAG      1488
Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu Asn Gln
                485                 490                 495

GCT TGG CAT GTC GGT TAC GAC ATT ACT TCC GGC TAC CGT GTC CCC AAT      1536
Ala Trp His Val Gly Tyr Asp Ile Thr Ser Gly Tyr Arg Val Pro Asn
            500                 505                 510

GCG TCC GAA GTG TAT TTC ACT TAC AAC CAC GGT TCG GGT AAT TGG CTG      1584
Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Asn Trp Leu
        515                 520                 525

CCC AAT CCC AAC CTG AAA GCC GAG CGC AGC ACC ACC CAC ACC CTG TCT      1632
Pro Asn Pro Asn Leu Lys Ala Glu Arg Ser Thr Thr His Thr Leu Ser
    530                 535                 540

CTG CAA GGC CGC AGC GAA AAA GGT ACT TTG GAT GCC AAC CTG TAT CAA      1680
Leu Gln Gly Arg Ser Glu Lys Gly Thr Leu Asp Ala Asn Leu Tyr Gln
545                 550                 555                 560

AAC AAT TAC CGC AAC TTC TTG TCT GAA GAG CAG AAG CTG ACC ACC AGC      1728
Asn Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Lys Leu Thr Thr Ser
                565                 570                 575
```

FIG. 9G


```
GGC GAT GTC GGC TGT ACT CAG ATG AAT TAC TAC TAC GGT ATG TGT AGC      1776
Gly Asp Val Gly Cys Thr Gln Met Asn Tyr Tyr Tyr Gly Met Cys Ser
            580                 585                 590

AAT CCT TAT TCC GAA AAA CCG GAA TGG CAG ATG CAA AAT ATC GAT AAG      1824
Asn Pro Tyr Ser Glu Lys Pro Glu Trp Gln Met Gln Asn Ile Asp Lys
        595                 600                 605

GCC CGA ATC CGT GGT CTT GAG CTG ACA GGC CGT CTG AAT GTG ACA AAA      1872
Ala Arg Ile Arg Gly Leu Glu Leu Thr Gly Arg Leu Asn Val Thr Lys
    610                 615                 620

GTA GCG TCT TTT GTT CCT GAG GGC TGG AAA TTG TTC GGC TCG CTG GGT      1920
Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser Leu Gly
625                 630                 635                 640

TAT GCG AAA AGC AAA CTG TCG GGC GAC AAC AGC CTG CTG TCC ACA CAG      1968
Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Ser Thr Gln
                645                 650                 655

CCG CCG AAA GTG ATT GCC GGT GTC GAC TAC GAA AGC CCG AGC GAA AAA      2016
Pro Pro Lys Val Ile Ala Gly Val Asp Tyr Glu Ser Pro Ser Glu Lys
            660                 665                 670
```

FIG. 9H


```
TGG GGT GTG TTC TCC CGC CTG ACT TAT CTG GGT GCG AAA AAG GCC AAA      2064
Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys Ala Lys
        675                 680                 685

GAC GCG CAA TAC ACC GTT TAT GAA AAC AAG GGC CGG GGT ACG CCT TTG      2112
Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Arg Gly Thr Pro Leu
    690                 695                 700

CAG AAA AAG GTA AAA GAT TAC CCG TGG CTG AAC AAG TCG GCT TAT GTG      2160
Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala Tyr Val
705                 710                 715                 720

TTT GAT ATG TAC GGC TTC TAC AAA CTG GCT AAA AAC CTG ACT TTG CGT      2208
Phe Asp Met Tyr Gly Phe Tyr Lys Leu Ala Lys Asn Leu Thr Leu Arg
                725                 730                 735

GCA GGC GTA TAT AAT GTG TTC AAC CGC AAA TAC ACC ACT TGG GAT TCC      2256
Ala Gly Val Tyr Asn Val Phe Asn Arg Lys Tyr Thr Thr Trp Asp Ser
            740                 745                 750

CTG CGC GGT TTG TAT AGC TAC AGC ACC ACC AAC GCG GTC GAC CGA GAT      2304
Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ala Val Asp Arg Asp
        755                 760                 765
```

FIG. 9I


```
GGC AAA GGC TTA GAC CGC TAC CGC GCC TCA GGC CGT AAT TAC GCC GTA      2352
Gly Lys Gly Leu Asp Arg Tyr Arg Ala Ser Gly Arg Asn Tyr Ala Val
    770                 775                 780

TCG CTG GAT TGG AAG TTT TGA ATTCC                                  2378
Ser Leu Asp Trp Lys Phe  *
785                 790
```

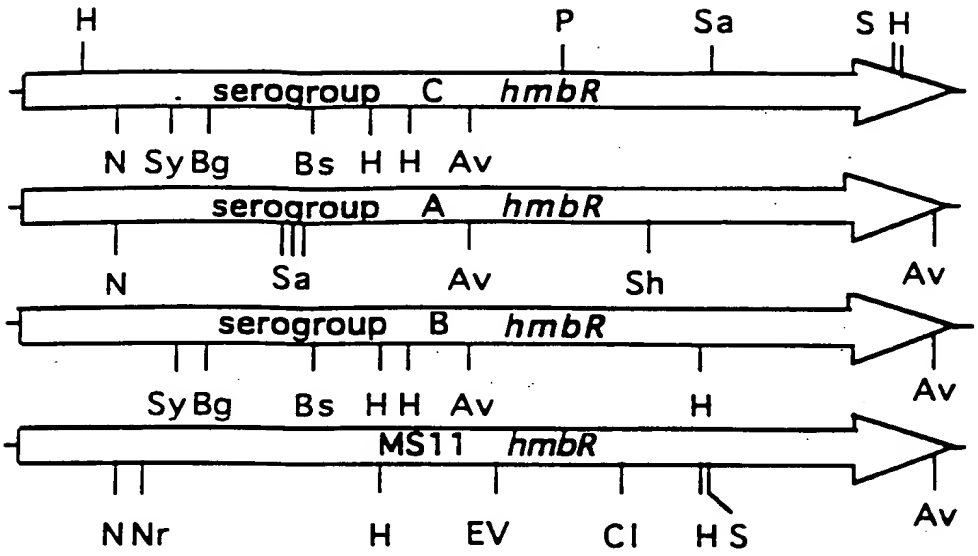

Figure 10

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FIG. 11A


```
HMBRA        MKPLQMLPIAALVGSIFGNPVLAADEAATETTPVKAEIKAVRVKGQRNAP   50
HMBRB        MKPLQMPPIAALLGSIFGNPVFAXDEAATETTPVKAEVKAVRVKGQRNAP   50
HMBRC        MKPLQMLPIAALVGSIFGNPVFAADEAATETTPVKAEVKAVRVKGQRNAP   50
HMBRMS11     MKPLHMLPIAALVGSIFGNPVLAADEAATETTPVKAEIKEVRVKDQLNAP   50
             ****.* *****.********.* ************.*.****.* ***

HMBRA        AAVERVNLNRIKQEMIRDNKDLVRYSTDVGLSDSGRHQKGFAVRGVEGNR  100
HMBRB        AAVERVNLNRIKQEMIRDNKDLVRYSTDVGLSDRSRHQKGFAIRGVEGDR  100
HMBRC        AAVERVNLNRIKQEMIRDNKDLVRYSTDVGLSDSGRHQKGFAVRGVEGNR  100
HMBRMS11     ATVERVNLGRIQQEMIRDNKDLVRYSTDVGLSDSGRHQKGFAVRGVEGNR  100
             *.******.**.**********************..*******.*****.*

HMBRA        VGVSIDGVNLPDSEENSLYARYGNFNSSRLSIDPELVRNIEIVKGADSFN  150
HMBRB        VGVSIDGVNLPDSEENSLYARYGNFNSSRLSIDPELVRNIDIVKGADSFN  150
HMBRC        VGVSIDGVNLPDSEENSLYARYGNFNSSRLSIDPELVRNIDIVKGADSFN  150
HMBRMS11     VGVSIDGVSLPDSEENSLYARYGNFNSSRLSIDPELVRNIEIAKGADSFN  150
             ********.*********************************.*.*******

HMBRA        TGSGALGGGVNYQTLQGRDLLLDDRQFGVMMKNGYSTRNREWTNTLGFGV  200
HMBRB        TGSGALGGGVNYQTLQGRDLLLPERQFGVMMKNGYSTRNREWTNTLGFGV  200
HMBRC        TGSGALGGGVNYQTLQGRDLLLPERQFGVMMKNGYSTRNREWTNTLGFGV  200
HMBRMS11     TGSGALGGGVNYQTLQGHDLLLDDRQFGVMMKNGYSSRNREWTNTLGFGV  200
             ******************.****  .************.************
```

FIG. 11B


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HMBRA        SNDRVDAALLYSQRRGHETESAGNRGYPVEGAGKETNIRGSARGIPDPSK  250
HMBRB        SNDRVDAALLYSQRRGHETESAGKRGYPVEGAGSGANIRGSARGIPDPSQ  250
HMBRC        SNDRVDAALLYSQRRGHETESAGKRGYPVEGAGSGANIRGSARGIPDPSQ  250
HMBRMS11     SNDRVDAALLYSQRRGHETESAGERGYPVEGAGSGAIIRGSSRGIPDPSK  250
             **********************.*********... ****.*******.

HMBRA        HKYHNFLGKIAYQINDNHRIGASLNGQQGHNYTVEESYNLTASSWREADD  300
HMBRB        HKYHSFLGKIAYQINDNHRIGASLNGQQGHNYTVEESYNLLASYWREADD  300
HMBRC        HKYHSFLGKIAYQINDNHRIGASLNGQQGHNYTVEESYNLLASYWREADD  300
HMBRMS11     HKYHNFLGKIAYQINDKHRIGPSFNGQQGHNYTIEESYNLTASSWREADD  300
             ****.***********.****.*.*********.****** ** ******

HMBRA        VNRRRNANLFYEWMPDSNWLSSLKADFDYQKTKVAAIN-KGSFPT-NYTT  348
HMBRB        VNRRRNTNLFYEWTPESDRLSMVKADVDYQKTKVSAVNYKGSFPT-NYTT  349
HMBRC        VNRRRNTNLFYEWTPESDRLSMVKADVDYQKTKVSAVNYKGSFPIEDSST  350
HMBRMS11     VNRRRNANLFYEWTPDSNWLSSLKADFDYQTTKVAAVNNKGSFPTD-YST  349
             ******.****** *.*..** .*** ***.***.*.* *****.   .*

HMBRA        WETEYHKKEVGEIYNRSMDTRFKRFTLRLDSHPLQLGGGRHRLSFKTFAS  398
HMBRB        WETEYHKKEVGEIYNRSMDTTFKRITLRMDSHPLQLGGGRHRLSFKTFAG  399
HMBRC        LTRNYNQKDLDEIYNRSMDTRFKRITLRLDSHPLQLGGGRHRLSFKTFAS  400
HMBRMS11     WTRNYNQKDLENIYNRSMDTRFKRFTLRMDSQPLQLGG-RHRLSLKTFAS  398
              . .*..*....******** ***.***.**.****** .****.****.
```

FIG. 11C


```
HMBRA          RRDFENLNRDDYYFSGRVVRTTSSIQHPVKTTNYGFSLSDQIQWNDVFSS  448
HMBRB          QRDFENLNRDDYYFSGRVVRTTNSIQHPVKTTNYGFSLSDQIQWNDVFSS  449
HMBRC          RRDFENLNRDDYYFSGRVVRTTSSIQHPVKTTNYGFSLSDQIQWNDVFSS  450
HMBRMS11       RREFENLNRDDYYFSERVSRTTSSIQHPVKTTNYGFSLSDQIQWNDVFSS  448
               .*.***********.** ***.**************************

HMBRA          RAGIRYDHTKMTPQELNAECHACDKTPPAANTYKGWSGFVGLAAQLNQAW  498
HMBRB          RAGIRYDHTKMTPQELNADCHACDKTPPAANTYKGWSGFVGLAAQLSQTW  499
HMBRC          RAGIRYDHTKMTPQELNAECHACDKTPPAANTYKGWSGFVGLAAQLNQAW  500
HMBRMS11       RADIRYDHTKMTPQELNADCHACDKTPPAANTYKGWSGFVGLAAQLNQAW  498
               **.***************.****************************.*.*

HMBRA          RVGYDITSGYRVPNASEVYFTYNHGSGNWLPNPNLKAERSTTHTLSLQGR  548
HMBRB          RVGYDVTSGFRVPNASEVYFTYNHGSGTWKPNPNLKAERSTTHTLSLQGR  549
HMBRC          RVGYDITSGYRVPNASEVYFTYNHGSGNWLPNPNLKAERTTTHTLSLQGR  550
HMBRMS11       HVGYDITSGYRVPNASEVYFTYNHGSGNWLPNPNLKAERSTTHTLSLQGR  548
               ..***.***.******************.* *********.**********

HMBRA          SEKGMLDANLYQSNYRNFLSEEQKLTTSGTPGCTEENAYYSICSDPYKEK  598
HMBRB          GDKGTLDANLYQSNYRNFLSEEQNLTVSGTPGCTEEDAYYYRCSDPYKEK  599
HMBRC          SEKGTLDANLYQSNYRNFLSEEQKLTTSGDVSCTQMNYYYGMCSNPYSEK  600
HMBRMS11       SEKGTLDANLYQNNYRNFLSEEQNLTTSGDVGCTQMNYYYGMCSNPYSEK  598
               ..** *******.**********.**.**. .**. . **  **.**.**
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FIG. 11D

```
HMBRA       LDWQMKNIDKARIRGIELTGRLNVDKVASFVPEGWKLFGSLGYAKSKLSG  648
HMBRB       LDWQMKNIDKARIRGIELTGRLNVDKVASFVPEGWKLFGSLGYAKSKLSG  649
HMBRC       LDWQMQNIDKARIRGLELTGRLNVDKVASFVPEGWKLFGSLGYAKSKLSG  650
HMBRMS11    PEWQMQNIDKARIRGLELTGRLNVTKVASFVPEGWKLFGSLGYAKSKLSG  648
             .***.*********.********.*************************

HMBRA       DNSLLSTQPLKVIAGIDYESPSEKWGVFSRLTYLGAKKVKDAQYTVYENK  698
HMBRB       DNSLLSTQPLKVIAGIDYESPSEKWGVFSRLTYLGAKKVKDAQYTVYENK  699
HMBRC       DNSLLSTQPLKVIAGIDYESPSEKWGVFSRLTYLGAKKVKDAQYTVYENK  700
HMBRMS11    DNSLLSTQPPKVIAGVDYESPSEKWGVFSRLTYLGAKKAKDAQYTVYENK  698
            ********* *****.**********************.***********

HMBRA       GWGTPLQKKVKDYPWLNKSAYVFDMYGFYKPVKNLTLRAGVYNLFNRKYT  748
HMBRB       GWGTPLQKKVKDYPWLNKSAYVFDMYGFYKPAKNLTLRAGVYNLFNRKYT  749
HMBRC       GWGTPLQKKVKDYPWLNKSAYVFDMYGFYKPVKNLTLRAGVYNVFNRKYT  750
HMBRMS11    GRGTPLQKKVKDYPWLNKSAYVFDMYGFYKLAKNLTLRAGVYNVFNRKYT  748
            *.***************************** .***********.******

HMBRA       TWDSLRGLYSYSTTNAVDRDGKGLDRYRAPGRNYAVSLEWKF          790
HMBRB       TWDSLRGLYSYSTTNAVDRDGKGLDRYRAPGRNYAVSLEWKF          791
HMBRC       TWDSLRGLYSYSTTNSVDRDGKGLDRYRAPSRNYAVSLEWKF          792
HMBRMS11    TWDSLRGLYSYSTTNAVDRDGKGLDRYRASGRNYAVSLDWKF          790
            ***************.*************..*******.***
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